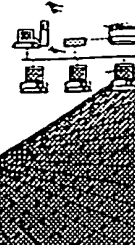


N. Brannan

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

RE-RUN

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/582,719B
Source: 1600
Date Processed by STIC: 11/23/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09 582,719B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003

TIME: 07:46:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

5 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
9 <120> TITLE OF INVENTION: Novel Sequence Variants of the Human Beta 2-Adrenergic
10 Receptor Gene and Use Thereof
14 <130> FILE REFERENCE: 101195-2
18 <140> CURRENT APPLICATION NUMBER: US 09/582,719B
C--> 20 <141> CURRENT FILING DATE: 2000-08-22
24 <150> PRIOR APPLICATION NUMBER: PCT/DE98/03818
26 <151> PRIOR FILING DATE: 1998-12-30
30 <150> PRIOR APPLICATION NUMBER: DE 197 58 401.2
32 <151> PRIOR FILING DATE: 1997-12-30
36 <160> NUMBER OF SEQ ID NOS: 23
40 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

44 <210> SEQ ID NO: 1
46 <211> LENGTH: 3451
48 <212> TYPE: DNA
50 <213> ORGANISM: human genomic clone
54 <220> FEATURE:
56 <221> NAME/KEY: mutation
58 <222> LOCATION: (1)..(3451)
60 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
61 mutation
62 s in positions 159, 245, 565, 934, 1120, 1221, 1541, 1568,
63 1633,
W--> 64 1666, 1839, 2078, 2110, 2640, 2826
68 <400> SEQUENCE: 1
E--> 69 cccgggttca agagattctc ctgtctcagc ctcccagta gctgggacta caggtagctg
70 60
E--> 72 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
73 120
E--> 75 aggatctttt gctttctata gttcaaaat gttcttaatg ttaagacatt cttaatactc
76 180
E--> 78 tgaaccatat gaatttgcca ttttggttaag tcacagacgc cagatggtgg caatttcaca
79 240
E--> 81 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
82 300
E--> 84 ttgggtttac tgaagaaatt gtttgaattc tcattgcac tccagttcaa cagataatga
85 360
E--> 87 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
88 420

*Whapped nucleics throughout = See error
Summary sheet item 1*

RAW SEQUENCE LISTING

DATE: 01/23/2003

PATENT APPLICATION: US/09/582,719B

TIME: 07:46:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

E--> 238 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
239 3420

E--> 241 gagtgtgtt gctcccccct ctggaaaccg c
242 3451

245 <210> SEQ ID NO: 2
247 <211> LENGTH: 3451
249 <212> TYPE: DNA
251 <213> ORGANISM: human genomic clone
255 <220> FEATURE:
257 <221> NAME/KEY: mutation
259 <222> LOCATION: (1)..(3451)
261 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
262 mutation
263 s in positions 1541, 1633, 1666
267 <400> SEQUENCE: 2

E--> 268 cccgggttca agagattctc ctgtctcagc ctcccagta gctgggacta caggtagctg
269 60

E--> 271 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
272 120

E--> 274 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt ctttaatactc
275 180

E--> 277 tgaaccatat gaatttgcca ttttggttaag tcacagacgc cagatggtgg caatttcaca
278 240

E--> 280 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
281 300

E--> 283 ttgggtttac tgaagaaatt gtttgaattc tcattgcac tcagttcaa cagataatga
284 360

E--> 286 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
287 420

E--> 289 cacacaaatt tctctctctg tcccaaaata catacttgca taccctcgct ccagataaaa
290 480

E--> 292 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggaggggcacc taaagtactt
293 540

E--> 295 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
296 600

E--> 298 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
299 660

E--> 301 gctcgggtga ggcaagttcg gagtaccag atggagacat ccgtgtctgt gtcgctctgg
302 720

E--> 304 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
305 780

E--> 307 ggtgcttctg tgtttgtttc tggccgcgtt tctgtgttgg acaggggtga ctttgtgccg
308 840

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311 900

E--> 313 tcagtgtcta tggctgtggt tcggtataag tctgagcatg tctgccaggg tgtattttgtg
314 960

E--> 316 cctgtatgtg cgtgcctcgg tgggcactct cgtttccttc cgaatgtggg gcagtgcgg
317 1020

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
393 2520
E--> 395 aattggatag gctatgtcaa ttctggtttc aatcccccta tctactgccg gagcccagat
396 2580
E--> 398 ttcaggattg ccttccagga gcttctgtgc ctgcgcaggt cttctttgaa ggcctatggg
399 2640
E--> 401 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
402 2700
E--> 404 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
405 2760
E--> 407 ggtactgtgc ctagegataa cattgattca caagggagga attgtagtac aaatgactca
408 2820
E--> 410 ctgctgtaaa gcagtttttc tacttttaaa gacccccccc cccccaacag aacactaaac
411 2880
E--> 413 agactattta acttgagggt aataaactta gaataaaaatt gtaaaaattg tatagagata
414 2940
E--> 416 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
417 3000
E--> 419 acttatttga gtgattattt gttatttga cagttcagtt cctctttgca tggaatttgt
420 3060
E--> 422 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
423 3120
E--> 425 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
426 3180
E--> 428 gtatctgaag gagattttcc ttcctacacc cttggacttg aggattttga gtatctcgga
429 3240
E--> 431 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgcacac acgggggtatt
432 3300
E--> 434 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
435 3360
E--> 437 agtaaataaa atgtttgacc atgccttcat tgcaacctgtt tgtccaaaac cccttgactg
438 3420
E--> 440 gagtgtgtgt gcctccccca ctggaaaccg c
441 3451
444 <210> SEQ ID NO: 3
446 <211> LENGTH: 3451
448 <212> TYPE: DNA
450 <213> ORGANISM: human genomic clone
454 <220> FEATURE:
456 <221> NAME/KEY: mutation
458 <222> LOCATION: (1)..(3451)
460 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
461      mutatio
462      ns in positions 1541, 1633, 1666
466 <400> SEQUENCE: 3
E--> 467 cccgggttca agagattctc ctgtctcagc ctcccagta gctgggacta caggtacgtg
468 60
E--> 470 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
471 120
E--> 473 aggatctttt gctttctata gcttcaaat gttcttaatg ttaagacatt cttaatactc
```

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
621 3120
E--> 623 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggttaattt
624 3180
E--> 626 gtatctgaag gagattttcc ttctacacc cttggacttg aggattttga gtatctcgga
627 3240
E--> 629 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acgggggtattt
630 3300
E--> 632 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
633 3360
E--> 635 agtaaataga atgtttgacc atgccttcac tgcacctgtt tgtccaaaac cccttgactg
636 3420
E--> 638 gagtgtgtgt gcttccccca ctggaaaccg c
639 3451
642 <210> SEQ ID NO: 4
644 <211> LENGTH: 3451
646 <212> TYPE: DNA
648 <213> ORGANISM: human genomic clone
652 <220> FEATURE:
654 <221> NAME/KEY: mutation
656 <222> LOCATION: (1)..(3451)
658 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
659 mutation
660 s in positions 1541, 1633, 1666
664 <400> SEQUENCE: 4
E--> 665 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtaactg
666 60
E--> 668 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
669 120
E--> 671 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
672 180
E--> 674 tgaaccatat gaatttgcca ttttggttaag tcacagacgc cagatggttg caatttcaca
675 240
E--> 677 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt ttagttttca
678 300
E--> 680 ttgggtttac tgaagaaatt gtttgaattc tcattgcac tcagttcaa cagataatga
681 360
E--> 683 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
684 420
E--> 686 cacacaactt tctctctctg tccaaaata catacttgca taccctcgct ccagataaaa
687 480
E--> 689 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
690 540
E--> 692 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
693 600
E--> 695 atgtttgaaa ggaatacac tgggttacog ggtgtatgtt gggaggggag cattatcagt
696 660
E--> 698 gctcgggtga ggcaagtto gagtaccag atggagacat ccgtgtctgt gtcgctctgg
699 720
E--> 701 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
```

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

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E--> 776 ctggtgatca tgggtotcgt ctactccagg gtctttcagg aggccaaaag gcagctccag
      777 2280
E--> 779 aagattgaca aatctgaggg ccgcttccat gtccagaacc ttagccagggt ggagcaggat
      780 2340
E--> 782 gggcggaagg ggcattgact ccgcagatct tccaagttct gcttgaagga gcacaaagcc
      783 2400
E--> 785 ctcaagacgt taggcatcat catgggcact ttcacctct gctggctgcc cttcttcac
      786 2460
E--> 788 gttaacattg tgcattgat ccaggataac ctcatccgta aggaagtta catcctccta
      789 2520
E--> 791 aattggatag gctatgtcaa ttctggtttc aatcccccta tctactgccg gagcccagat
      792 2580
E--> 794 ttcaggattg cttccaggga gcttctgtgc ctgcgcagggt cttctttgaa ggcctatggg
      795 2640
E--> 797 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
      798 2700
E--> 800 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
      801 2760
E--> 803 ggtactgtgc ctagcgataa cattgattca caagggagga attgtagtac aaatgactca
      804 2820
E--> 806 ctgctgtaaa gcagtttttc tacttttaaa gacccccccc cccccaacag aacactaaac
      807 2880
E--> 809 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
      810 2940
E--> 812 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
      813 3000
E--> 815 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tgggaattgt
      816 3060
E--> 818 aagtttatgt ctaaagagct ttagtcctag aggacctgag totgctatat ttcatgact
      819 3120
E--> 821 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
      822 3180
E--> 824 gtatctgaag gagattttcc ttccctacacc cttggacttg aggattttga gtatctcgga
      825 3240
E--> 827 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgcctac acgggggtatt
      828 3300
E--> 831 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaagggtc taaagtttac
      832 3360
E--> 834 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
      835 3420
E--> 837 gagtgtgtgt gcctccccca ctggaaaccg c
      838 3451
841 <210> SEQ ID NO: 5
843 <211> LENGTH: 3451
845 <212> TYPE: DNA
847 <213> ORGANISM: human genomic clone
851 <220> FEATURE:
853 <221> NAME/KEY: mutation
855 <222> LOCATION: (1)..(3451)
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003

TIME: 07:46:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

857 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
858 mutation
859 s in positions 1541, 1568, 1633, 1666
863 <400> SEQUENCE: 5

E--> 864 cccgggttca agagattctc ctgtctcagc ctcccagagta gctgggacta cagggtacgtg
865 60
E--> 867 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
868 120
E--> 870 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttaatactc
871 180
E--> 873 tgaaccatat gaatttgcca ttttggttaag tcacagacgc cagatgggtg caatttcaca
874 240
E--> 876 tggcacaacc cgaaagatta acaaaactatc cagcagatga aaggattttt tttagtttca
877 300
E--> 879 ttgggtttac tgaagaaatt gtttgaattc tcattgcatc tccagttcaa cagataatga
880 360
E--> 882 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
883 420
E--> 885 cacacaactt tctctctctg tcccaaaata catacttgca tcccccgct ccagataaaa
886 480
E--> 888 tccaaaggtt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
889 540
E--> 891 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
892 600
E--> 894 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
895 660
E--> 897 gctcgggtga ggcaagtctg gactaccag atggagacat ccgtgtctgt gtcgtctctg
898 720
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901 780
E--> 903 ggtgcttctg tgtttgtttc tggccgcgtt tctgtgttg acaggggtga ctttgtgcgc
904 840
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907 900
E--> 909 tcagtgtcta tggctgtggt tcggtataag tctgagcatg tctgccaggg tgtatttctg
910 960
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913 1020
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916 1080
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919 1140
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922 1200
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925 1260
E--> 927 gagtgcctcg ccccttcgcg gctgccggcg tgccattggc cgaaagtcc cgtacgtcac
928 1320
E--> 930 ggcgagggca gttcccctaa agtcctgtgc acataacggg cagaacgcac tgcgaagcgg

RAW SEQUENCE LISTING

DATE: 01/23/2003

PATENT APPLICATION: US/09/582,719B

TIME: 07:46:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

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E--> 1005 ctgctgtaaa gcagtttttc tactttttaa gacccccccc cccccaag aacactaac
      1006 2880
E--> 1008 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
      1009 2940
E--> 1011 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
      1012 3000
E--> 1014 acttatttga gtgattatgt gttatttgta cagttcagtt cctctttgca tggatttgt
      1015 3060
E--> 1017 aagtttatgt ctaaagagct ttagtcttag aggacctgag tctgctatat tttcatgact
      1018 3120
E--> 1020 tttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaattt
      1021 3180
E--> 1023 gtatctgaag gagattttcc ttctacacc cttggacttg aggattttga gtatctcgga
      1024 3240
E--> 1026 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acggggtatt
      1027 3300
E--> 1029 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
      1030 3360
E--> 1032 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
      1033 3420
E--> 1035 gagtgtgtgt gcctccccca ctggaaaccg c
      1036 3451
      1039 <210> SEQ ID NO: 6
      1041 <211> LENGTH: 3451
      1043 <212> TYPE: DNA
      1045 <213> ORGANISM: human genomic clone
      1049 <220> FEATURE:
      1051 <221> NAME/KEY: mutation
      1053 <222> LOCATION: (1)..(3451)
      1055 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
      1056 mutation
      1057 s in positions 1541, 1568, 1633, 1666
      1061 <400> SEQUENCE: 6
E--> 1062 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta caggtaoctg
      1063 60
E--> 1065 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
      1066 120
E--> 1068 aggatctttt gctttctata gttcaaaat gttcttaaag ttaagacatt cttaatactc
      1069 180
E--> 1071 tgaaccatat gaatttgcca ttttgtaag tcacagacgc cagatggtgg caatttcaca
      1072 240
E--> 1074 tggcgcaacc cgaaagatta acaaactatc cagcagatga aaggattttt tttagtttca
      1075 300
E--> 1077 ttgggtttac tgaagaaatt gtttgaattc tcattgcac tcagttcaa cagataatga
      1078 360
E--> 1080 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
      1081 420
E--> 1083 cacacaactt tctctctctg tcccaaaata catacttgca taccctcgct ccagataaaa
      1084 480
```

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

E--> 1234 gagtgctgtt gcctcccca ctggaaccg c
1235 3451
1238 <210> SEQ ID NO: 7
1240 <211> LENGTH: 3451
1242 <212> TYPE: DNA
1244 <213> ORGANISM: human genomic clone
1248 <220> FEATURE:
1250 <221> NAME/KEY: mutation
1252 <222> LOCATION: (1)..(3451)
1254 <223> OTHER INFORMATION: variant of the human beta2-adrenergic receptor gene with
1255 mutation
1256 s in positions 1541, 1568, 1633, 1666
1260 <400> SEQUENCE: 7
E--> 1261 cccgggttca agagattctc ctgtctcagc ctcccgagta gctgggacta cagggtacgtg
1262 60
E--> 1264 ccaccacacc tggctaattt ttgtattttt agtagagaca agagttacac catattggcc
1265 120
E--> 1267 aggatctttt gctttctata gcttcaaaat gttottaatg ttaagacatt cttaatactc
1268 180
E--> 1270 tgaaccatat gaatttgcca ttttggttaag tcacagacgc cagatggtgg caatttcaca
1271 240
E--> 1273 tggcacaacc cgaaagatta acaaactatc cagcagatga aaggattttt ttagtttca
1274 300
E--> 1276 ttgggtttac tgaagaaatt gtttgaattc tcattgcac tccagttcaa cagataatga
1277 360
E--> 1279 gtgagtgatg ccacactctc aagagttaaa aacaaaacaa caaaaaaatt aaaacaaaag
1280 420
E--> 1282 cacacaactt totctctctg tcccaaaata catacttgca taccctcgct ccagataaaa
1283 480
E--> 1285 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt
1286 540
E--> 1288 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa
1289 600
E--> 1291 atgtttgaaa gggaatacac tgggttaccg ggtgtatgtt gggaggggag cattatcagt
1292 660
E--> 1294 gctcgggtga ggcaagttcg gagtaccag atggagacat ccgtgtctgt gtcgctctgg
1295 720
E--> 1297 atgcctccaa gccagcgtgt gtttactttc tgtgtgtgtc accatgtctt tgtgcttctg
1298 780
E--> 1300 ggtgcttctg tgtttgtttc tggccgcgtt tctgtgttgg acaggggtga ctttgtgccg
1301 840
E--> 1303 gatggttct gtgtgagagc gcgcgcgagt gtgcatgtcg gtgagctggg aggggtgtgc
1304 900
E--> 1306 tcagtgtcta tggctgtggt tcggtataag tctgagcatg tctgccaggg tgtatttctg
1307 960
E--> 1309 cctgtatgtg cgtgcctcgg tgggcactct cgtttccttc cgaatgtggg gcagtgccg
1310 1020
E--> 1312 tgtgctgccc tctgccttga gacctcaagc cgcgcaggcg ccagggcag gcaggtagcg
1313 1080

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

```
1388 2580
E--> 1390 ttcaggattg ccttccagga gcttctgtgc ctgcgcaggt cttctttgaa ggcctatggg
1391 2640
E--> 1393 aatggctact ccagcaacgg caacacaggg gagcagagtg gatatcacgt ggaacaggag
1394 2700
E--> 1396 aaagaaaata aactgctgtg tgaagacctc ccaggcacgg aagactttgt gggccatcaa
1397 2760
E--> 1399 ggtactgtgc ctagegataa cattgattca caagggagga attgtagtac aaatgactca
1400 2820
E--> 1402 ctgctgtaaa gcagtttttc tacttttaaa gacccccccc cccccaacag aacactaaac
1403 2880
E--> 1405 agactattta acttgagggt aataaactta gaataaaatt gtaaaaattg tatagagata
1406 2940
E--> 1408 tgcagaagga agggcatcct tctgcctttt ttattttttt aagctgtaaa aagagagaaa
1409 3000
E--> 1411 acttatttga gtgattattt gttatttgta cagttcagtt cctctttgca tggaatttgt
1412 3060
E--> 1414 aagtttatgt ctaaagagct ttagtcctag aggacctgag tctgctatat tttcatgact
1415 3120
E--> 1417 ttccatgta tctacctcac tattcaagta ttaggggtaa tatattgctg ctggtaat
1418 3180
E--> 1420 gtatctgaag gagattttcc ttctacacc cttggacttg aggatttga gtatctcgga
1421 3240
E--> 1423 cctttcagct gtgaacatgg actcttcccc cactcctctt atttgctcac acgggggtatt
1424 3300
E--> 1426 ttaggcaggg atttgaggag cagcttcagt tgttttcccg agcaaaggtc taaagtttac
1427 3360
E--> 1429 agtaaataaa atgtttgacc atgccttcat tgcacctgtt tgtccaaaac cccttgactg
1430 3420
E--> 1432 gagtgtgtgt gctccccca ctggaaaccg c
1433 3451
1436 <210> SEQ ID NO: 8
1438 <211> LENGTH: 27
1440 <212> TYPE: DNA
1442 <213> ORGANISM: Artificial
1446 <220> FEATURE:
1448 <221> NAME/KEY: primer_bind
1450 <222> LOCATION: (1)..(27)
1452 <223> OTHER INFORMATION: primer ADRBR-F1 for amplification of fragment I
1456 <400> SEQUENCE: 8
E--> 1457 tattggccag gatcttttgc tttctat
1458 27
1461 <210> SEQ ID NO: 9
1463 <211> LENGTH: 23
1465 <212> TYPE: DNA
1467 <213> ORGANISM: Artificial
1471 <220> FEATURE:
1473 <221> NAME/KEY: primer_bind
1475 <222> LOCATION: (1)..(23)
```

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

1477 <223> OTHER INFORMATION: primer ADRBR-R1 for amplification of fragment I
1481 <400> SEQUENCE: 9
E--> 1482 taacattaag aacattttga agc
1483 23
1486 <210> SEQ ID NO: 10
1488 <211> LENGTH: 22
1490 <212> TYPE: DNA
1492 <213> ORGANISM: Artificial
1496 <220> FEATURE:
1498 <221> NAME/KEY: primer_bind
1500 <222> LOCATION: (1)..(22)
1502 <223> OTHER INFORMATION: primer ADRBR-F2 for amplification of fragment II
1506 <400> SEQUENCE: 10
E--> 1507 gcataccccc gctccagata aa
1508 22
1511 <210> SEQ ID NO: 11
1513 <211> LENGTH: 24
1515 <212> TYPE: DNA
1517 <213> ORGANISM: Artificial
1522 <220> FEATURE:
1524 <221> NAME/KEY: primer_bind
1526 <222> LOCATION: (1)..(24)
1528 <223> OTHER INFORMATION: primer ADRBR-R2 for amplification of fragment II
1532 <400> SEQUENCE: 11
E--> 1533 gcacgcacat acaggcaciaa atac
1534 24
1537 <210> SEQ ID NO: 12
1539 <211> LENGTH: 19
1541 <212> TYPE: DNA
1543 <213> ORGANISM: Artificial
1547 <220> FEATURE:
1549 <221> NAME/KEY: primer_bind
1551 <222> LOCATION: (1)..(19)
1553 <223> OTHER INFORMATION: primer ADRBR-F3 for amplification of fragment III
1557 <400> SEQUENCE: 12
E--> 1558 ggccgcgttt ctgtgttgg
1559 19
1562 <210> SEQ ID NO: 13
1564 <211> LENGTH: 22
1566 <212> TYPE: DNA
1568 <213> ORGANISM: Artificial
1572 <220> FEATURE:
1574 <221> NAME/KEY: primer_bind
1576 <222> LOCATION: (1)..(22)
1578 <223> OTHER INFORMATION: primer ADRBR-R2 for amplification of fragment III
1582 <400> SEQUENCE: 13
E--> 1583 agtgcgttct gcccgttatg tg
1584 22
1587 <210> SEQ ID NO: 14

Input Set : A:\EP.txt
Output Set: N:\CRF4\01232003\I582719B.raw

1589 <211> LENGTH: 21
1591 <212> TYPE: DNA
1593 <213> ORGANISM: Artificial
1597 <220> FEATURE:
1599 <221> NAME/KEY: primer_bind
1601 <222> LOCATION: (1)..(21)
1603 <223> OTHER INFORMATION: primer ADRBR-F8 for amplification of fragment VIII
1607 <400> SEQUENCE: 14

E--> 1608 ggtactgtgc ctagcgataa c
1609 21
1612 <210> SEQ ID NO: 15
1614 <211> LENGTH: 28
1616 <212> TYPE: DNA
1618 <213> ORGANISM: Artificial
1622 <220> FEATURE:
1624 <221> NAME/KEY: primer_bind
1626 <222> LOCATION: (1)..(28)
1628 <223> OTHER INFORMATION: primer ADRBR-R8 for amplification of fragment VIII
1632 <400> SEQUENCE: 15

E--> 1633 taaaataccc cgtgtgagca aataagag
1634 28
1637 <210> SEQ ID NO: 16
1639 <211> LENGTH: 20
1641 <212> TYPE: DNA
1643 <213> ORGANISM: Artificial
1647 <220> FEATURE:
1649 <221> NAME/KEY: primer_bind
1651 <222> LOCATION: (1)..(20)
1653 <223> OTHER INFORMATION: primer ADRBR-F4 for amplification of fragment IV
1657 <400> SEQUENCE: 16

E--> 1658 ggggagggaa aggggaggag
1659 20
1662 <210> SEQ ID NO: 17
1664 <211> LENGTH: 21
1666 <212> TYPE: DNA
1668 <213> ORGANISM: Artificial
1672 <220> FEATURE:
1674 <221> NAME/KEY: primer_bind
1676 <222> LOCATION: (1)..(21)
1678 <223> OTHER INFORMATION: primer ADRBR-R4 for amplification of fragment IV
1682 <400> SEQUENCE: 17

E--> 1683 ctgccaggcc catgaccaga t
1684 21
1687 <210> SEQ ID NO: 18
1689 <211> LENGTH: 22
1691 <212> TYPE: DNA
1693 <213> ORGANISM: Artificial
1697 <220> FEATURE:
1699 <221> NAME/KEY: primer_bind

RAW SEQUENCE LISTING

DATE: 01/23/2003

PATENT APPLICATION: US/09/582,719B

TIME: 07:46:49

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

1701 <222> LOCATION: (1)..(22)

1703 <223> OTHER INFORMATION: primer ADRBR-F7 for amplification of fragment VII

1707 <400> SEQUENCE: 18

E--> 1708 ctggctgccc ttcttcacg tt

1709 22

1712 <210> SEQ ID NO: 19

1714 <211> LENGTH: 23

1716 <212> TYPE: DNA

1718 <213> ORGANISM: Artificial

1722 <220> FEATURE:

1724 <221> NAME/KEY: primer_bind

1726 <222> LOCATION: (1)..(23)

1728 <223> OTHER INFORMATION: primer ADRBR-R7 for amplification of fragment VII

1732 <400> SEQUENCE: 19

E--> 1733 taccctaagt taaatagtct gtt

1734 23

1737 <210> SEQ ID NO: 20

1739 <211> LENGTH: 17

1741 <212> TYPE: DNA

1743 <213> ORGANISM: Artificial

1747 <220> FEATURE:

1749 <221> NAME/KEY: primer_bind

1751 <222> LOCATION: (1)..(17)

1753 <223> OTHER INFORMATION: primer ADRBR-F5 for amplification of fragment V

1757 <400> SEQUENCE: 20

E--> 1758 atgcgcgga ccacgac

1759 17

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/582,719B

DATE: 01/23/2003

TIME: 07:46:50

Input Set : A:\EP.txt

Output Set: N:\CRF4\01232003\I582719B.raw

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:64 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:268 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
M:254 Repeated in SeqNo=2
L:467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:665 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
M:254 Repeated in SeqNo=4
L:864 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
M:254 Repeated in SeqNo=5
L:1062 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
M:254 Repeated in SeqNo=6
L:1261 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7
L:1457 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:8
L:1482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:9
L:1507 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:10
L:1533 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:11
L:1558 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:12
L:1583 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:13
L:1608 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:14
L:1633 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:15
L:1658 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16
L:1683 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:17
L:1708 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:18
L:1733 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:19
L:1758 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:20
L:1783 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:21
L:1809 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:22
L:1835 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:23
M:254 Repeated in SeqNo=23